SYNOPSIS OF RESEARCH PROJECT

1. Name of the Student	**:**	Sanapala Sai Harshavardhan
2. Registration No.	**:**	1010125050
3. Faculty	**:**	Agriculture
4. Name of the Degree Submitted for	**:**	Ph. D.
5. Major Subject	**:**	Genetics and Plant Breeding
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7. Name of Major Guide	**:**	Dr. Lata J. Raval Professor Department of Genetics and Plant Breeding College of Agriculture, JAU., Junagadh
8. Title of Research Project/ Project Report	**:**	Genome-Wide Association Mapping and Stability Analysis for Root Rot Resistance and Seed Yield Related Traits in Sesame (*Sesamum indicum* L.)

9. **Introduction**

Sesame (*Sesamum indicum* L.) is a significant smallholder agricultural system oil seed crop that botanically, the plant falls under the family Pedaliaceae and genus Sesamum. Sesame is commonly referred to as til, gingelly, benne seed and simsim in other regions of the world (Muthoni and Shimelis, 2025). Sesame is a diploid plant (2n = 2x = 26), which is a warm-season crop with a high degree of adaptability to various agro-ecological factors (Najeeb *et al*., 2011). It has an erect growth habit, indeterminate flowering, comparatively short life cycle and has a high oil concentration ability in their seeds (Dissanayake, 2017).

Sesame seeds are very valued products that are consumed by humans because of the availability of oil and nutrient value. They find extensive application in all kinds of typical food preparation like roasting seeds, sweet, confectionery foodstuffs, cakes and biscuits and also used as part of chutneys, oils and other food cooking preparations (Wei *et al.,* 2022). Sesame seeds are good sources of high-quality edible oil as well as protein, vitamins and minerals. The crop has been characterized by its flexibility to a broad range of agro-climatical and can tolerate moderate drought conditions

(Abbas *et al.,* 2022). Sesame can grow in moderately low input low soil fertility conditions. Hence, farmers tend to prefer it due to its low cost and low risk crop and in the rain-fed and marginal farming environments.

India ranks among the leading producers of sesame. The crop was cultivated in the country during 2024-25 over an area of approximately 1,500 thousand hectares, yielding 866.11 thousand metric tonnes and yield levels average around 550 kg per hectare. (Anonymous, 2026).In Gujarat, the area under sesame cultivation was about 115.20 thousand hectares, producing approximately 123.49 thousand metric tonnes, with an average yield of 1072 kg per hectare during the same period of time (Anonymous, 2026). Major sesame-growing states of India include Gujarat, Rajasthan, Madhya Pradesh, Uttar Pradesh, Andhra Pradesh and West Bengal.

Macrophomina phaseolina is the cause of stem and root rot of sesame (Adhikary *et al.,* 2019). Initially, the disease was recognized through visual observation as the black surface appearance at the plant base and then spread vertically in its entire stem area (Ghosh *et al.,* 2018). Plant diseased roots were black in colour with fewer secondary rootlets. Browning is caused by capsule infection and results in drying and early opening of capsule. Later on, the affected plants turned black completely that led to wilting and defoliation of foliage (Khan and Javaid, 2023).

Despite significant advancements in sesame improvement programmes, the average productivity of the crop is significantly below its potential. Genetic variability present in the experimental material plays a vital role in determining the success of crop improvement programmes. Consequently, the nature and extent of hereditary variation must be carefully evaluated for effective selection. The effectiveness of the phenotypic selection used to improve the yield is also determined by the extent of genetic variation along with environmental influences governing the expression of different traits (Haussmann *et al*., 2004).

Seed yield in sesame is a quantitative character controlled by multiple genes and also affected by various component characters. These traits influence yield both directly and indirectly. Therefore, it is of great importance to understand the correlation between yield and its constituent characteristics in order to make the selection strategies effective. Correlation analysis provides basis for the major yield-contributing characters that can be identified and the necessary selection parameters for developing high-yielding genotypes (Bekele *et al*., 2025).

Stability of genotypes in differing environmental conditions is important in consistent performance across locations and seasons. Stability is an indication of genotype adaptive capacity for different environments. The main objective of plant breeding is to develop genotypes that perform well under specific or diverse environmental conditions (Simmonds, 1962). Nonetheless, interactions between genotypes and environments (G × E) influence phenotypic expression and complicate selection since genotype performance in one environment can differ in another Main and interaction effect sizes vary amongst genotypes and thus the G × E interactions require detailed analysis to determine the stable and high-performance genotypes across environments (Cooper and DeLacy, 1994).

Agro-morphological characteristics are not always sufficient to measure genetic diversity because they can be easily affected by the environment (Bahram *et al.*, 2014). Crop improvement programmes (Allard, 1960), especially in sesame are based on the efficient use of genetic diversity. In that regard, molecular markers including Simple Sequence Repeats (SSRs) are an effective method to determine genetic relationships among genotypes. The SSR markers are very informative because they have co-dominant inheritance are multi-allelic, highly polymorphic, and reproducible (Hernandez *et al.*, 2002). Their extensive presence, genome-wide distribution and high polymorphic information content (PIC) make them helpful in the assessment of genetic diversity and in marker-assisted selection (Gupta *et al.*, 2009).

Molecular technologies combined with traditional methods of crop breeding have huge potential in solving modern challenges of crop improvement. The contemporary research activities have been mainly concerned with identifying regions of the genome related to important characteristics to enable the process of Marker-Assisted Selection (MAS). Seed yield is a quantitative characteristic with continuous variation in the segregated population and open-pollinated populations that have been improved by selection, resulting in a higher frequency of favourable alleles at different loci. Traditional QTL mapping based on biparental populations has been effective in identifying genomic regions linked to various qualitative and quantitative traits, but its use has been limited by the low mapping resolution, which commonly ranges between 10 and 30 cM and includes only a few alleles segregating at a specific locus

Another approach is association mapping (AM), which is also referred to as genome-wide association studies (GWAS), which utilizes the broader genetic diversity

found in natural populations, historical germplasm and breeding lines. This method discovers historical recombination events over generations and thus makes it possible to achieve higher mapping resolution than traditional QTL mapping. It helps in the determination of genomic regions that are linked covering a wide variety of phenotypic traits. AM is commonly known as linkage disequilibrium (LD) mapping as it is based on the non-random association between alleles at separate loci. to identify the marker-trait associations, which makes it possible to do a large-scale analysis in unstructured and diverse populations (Morton, 2005; Slatkin, 2008). Identification of the molecular markers closely associated with with candidate genes or QTLs that regulate desired traits is also a critical step in the successful application of selection using molecular markers (Collard and Mackill, 2008).

10. Practical utility of the research project

Macrophomina phaseolina is the cause of root rot that is a major limitation to the production of sesame especially in drought-affected regions with high temperature conditions. Comparison of various types of sesame genotypes with this pathogen will give essential data on the degree of genetic variation in terms of resistance to the disease. The detection of both resistant and moderately resistant genotypes could be useful genetic materials in breeding programmes to come up with varieties that combine high yield with disease resistance and thus increase the stability of the yield in stressful environments.

Moreover, genotype characterization according to the response to *Macrophomina phaseolina* will make it easy to select appropriate parents to be used in hybridization and resistance breeding. The concerns of phenotypic screening can be further enhanced by incorporating the component of molecular approaches that will allow detecting resistance-related markers. The findings of the current research will help in building sustainable disease control measures involving host plants resistance, dependence on chemical practices will be cut and sustainable sesame production will be enhanced.

The current study is likely to produce detailed data on the magnitude of genetic diversity present in sesame, which is a primary prerequisite of effectiveness of any breeding programme. Determination of essential genetic parameters such as heritability and genetic advance gives useful insights concerning the nature of gene

action in which the important traits are governed. Such information will be helpful in determining the characters amenable to selection and will assist in developing effective strategies of population improvement and varietal development.

Understanding the association between yield and component traits is necessary to enhance production in sesame. The correlation analysis of various characters will help in determining the most significant traits that will contribute to seed yield. This information will help breeders to develop effective selection indices and, in this case, to improve multiple traits simultaneously. This will eventually make the selection process more effective by allowing indirect selection based on associated traits.

The Genotype × Environment (G × E) interactions will be evaluated and this will provide information on how the genotypes will perform in a particular environment. The fact that genotypes usually respond differently across environments makes it essential to select stable and high-yielding genotypes to maintain consistent crop productivity. The stability analysis will be used to aid the selection of genotypes that display consistent performance in different locations and seasons thereby enhancing adaptability and minimizing the risks associated with environmental fluctuations.

The application of molecular markers in the current experiment will permit precise assessment of genetic diversity among sesame genotypes. This will help in identification of genetically divergent parents for hybridization and increasing the probability of obtaining superior recombinants. Molecular characterization will also offer more insights into genetic relationships at the DNA level which cannot be accomplished at times using morphological characteristics. Such information can aid breeding programmes and promote the proper conservation and utilisation of genetic resources.

Moreover, the Genome-Wide Association Studies (GWAS) will be employed, which will enable the identification of significant marker trait associations and genomic regions controlling important agronomic traits. The technique makes use of historical recombination events and hence offers better mapping resolution compared to conventional QTL mapping. The detection of reliable molecular markers that are related to desirable traits will enhance the efficiency of Marker Assisted Selection (MAS) more effective. The overall effect of combining traditional breeding technologies with the latest molecular technologies is the rapid development of high

yielding, stable and adaptable sesame varieties, which will also help to enhance productivity and promote sustainable development of the agricultural development.

Genome-wide association studies (GWAS) have become an important tool for increasingly significant in wide range of agriculture crops, such as sesame, in recent years. Nonetheless, genotype panels that are used in GWAS are usually different in composition among studies. A wide array of genotypes was used in the current study, which will be obtained from the Agricultural Research Station, Amreli. Marker–trait association using GWAS aids breeding programmes through the application of marker-assisted selection (MAS), thereby improving the efficiency of breeding programmes more effective and precise than the traditional approaches for varietal development.

11. Objectives

In light of the above considerations, the present investigation was undertaken using 150 genotypes of sesame (*Sesamum indicum* L) in four environments (two seasons and two locations), with the following objectives.

1. To screen genotypes of sesame against *Macrophomina* root rot resistance
2. To determine the extent of genotypic and phenotypic variability, heritability and genetic advance for seed yield and yield attributing traits over the environments
3. To estimate of phenotypic and genotypic correlation coefficient for seed yield and its component traits
4. To assess the nature and magnitude of G × E interaction and phenotypic stability parameters of sesame genotypes over the environments
5. To study the extent of genetic and molecular diversity in sesame genotypes
6. To work out GWAS for root rot, seed yield and yield attributing traits in sesame genotypes using molecular markers

12. Review of Literature

Plant breeders are always concerned with the improvement of both quantitative and qualitative traits in nature. Therefore, proper understanding is required for the genetic structure of various important characters and knowledge of interrelationship among them. The literature available pertaining to variability, correlation, phenotypic stability, genetic and molecular diversity and genome wide association studies in sesame are review under the following sub-heads.

12.1 *Macrophomina* root rot resistance

12.2 Variability parameters

12.3 Correlation coefficients

12.4 Phenotypic stability analysis

12.5 Genetic diversity and molecular diversity

12.6 Genome wide association studies

12.1 *Macrophomina* root rot resistance

Ghias *et al.* (2021) 52 sesame varieties were investigated through a period of two years, and it was found that the Disease Infection percentage (DI%) of the studied types varied significantly between the two years. In addition, the data showed that DI% for genotypes tested in 2017 varied between 6.97% and 50.82%, while DI% for genotypes tested in 2018 maintained between 4.91% and 52.63%."

Ashfaq *et al.* (2023) examined fifty sesame genotypes in order to determine the source of resistance. *Macrophomina* stem/root rot disease and found that the incidence ranged from 65% to 100%. Out the fifty genotypes evaluated, FFAT 04 had the lowest root rot incidence (65%). "It had been found that none of the genotypes are immune. In a breeding program to create resistant varieties identified resistant genotypes can be used as parents."

"Pandey *et al.* (2023) conducted a research on one hundred three genotypes of sesame and observed that 11 genotypes namely S-0644, KMR-53, IS-1672, NIC-16256, IS-245, TC-30, IC-131943, EC-334974, NIC-7935, GRT-8245, and NIC-8439-B showed excellent performance with less disease incidence."

"Akshaya *et al.* (2026) evaluated a total of thirty-one sesame genotypes for resistance to *M. phaseolina* using both *in vitro* (paper towel) and *in vivo* (greenhouse pot culture) screening methods and observed that in-vitro screening effectively differentiated genotypes based on germination and infection levels with JCS-3751 and JCS4805 recording the highest germination (87–89%) and lowest infection (5.33–7.66%), followed by moderately resistant genotypes such as JCS-3287, JCS-4806, and GT-10. Under greenhouse conditions, these genotypes also exhibited higher germination and lower PDI (6.66–8.66%), confirming stable resistance across both screening methods. In contrast, susceptible genotypes

including JCS-4983, JCS4977, JCS-4962 and Swetha showed poor germination, severe seed rot and high seedling mortality under pathogen stress.

12.2 Variability parameters

In crop improvement programmes superior plants are selected from populations with genetic variability. It is a known fact that selection works effectively when the variation observed is heritable in nature. Thus, the degree of variation is determinant of the amount of progress achieved through selection. To develop an effective breeding programme for crop improvement, there is a need to estimate the heritability. The most common parameters used to assess genetic variability are Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), Heritability and Genetic Advance (Cobb *et al*.,2019).

Patidar *et al.* (2020) For study of genetic variability, heritability, and genetic advance 27 elite lines were examined. Except for yield per plot, all eleven traits showed highly significant variances. The number of seeds per capsule, internode length, and seed yield (kg/ha) all showed moderate levels of GCV and PCV values, suggesting that these traits contribute to genetic variability in a somewhat moderate way. Three characteristics (internode length, oil content, and number of seeds per capsule) had strong (80%) heritability. Internode length had the highest genetic advance percentage of mean, followed by seed yield (kg/ha) and the number of seeds per capsule.

Pavani *et al.* (2020) studied thirty sesame genotypes and significant genetic differences were found for each of the ten characters using analysis of variance High Phenotypic and Genotypic Coefficient of Variation were observed for the number of capsules per plant, while it was moderate for days to 50% flowering, plant heigh t to first capsule, number of branches per plant. On the other hand, height of the main stem, capsule length, 1000 seed weight, Low genotypic and phenotypic coefficients of variation were found in days to maturity, oil content, and yield of seed per plant. Days to 50% flowering, the number of branches per plant, and the height of the plant to the first capsule all showed high heritability and genetic advance as a percentage of mean, whereas the height of the main stem showed high heritability and moderate genetic advance as a percentage of mean.

Low genetic advancement and heritability as a percentage of mean capsule length, oil content, days to maturity, 1000 seed weight, and seed yield per plant.

Kumar *et al.* (2022) examined thirty-three sesame genotypes and it was found that analysis of variance showed substantial variations among the genotypes for all characteristics. For seed yield, the number of productive branches, and internode length, the Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were greater. Sesame genotypes showed greater genetic advancement as a percentage of mean for seed yield, number of productive branches, height of the first node from the ground, and internode length.

"Sasipriya *et al.* (2022) evaluated 51 sesame genotypes and observed that the characteristic 1000 seed weight showed the highest genotypic and phenotypic coefficient of variation among the different quantitative traits studied. For the following traits: days to 50% flowering, plant height, number of branches per plant, number of capsules per plant, number of seeds per capsule, and seed yield per plant, moderate estimates of genotypic and phenotypic coefficients of variation have been identified."

Gedifew *et al.* (2023) studied sixty-four sesame genotypes, comprising five varieties and fifty-nine accessions. He found that, apart from internode length and characteristics related to seed shattering, analysis of variance showed that sesame genotypes were significantly different for every character. Plant height to the first branch, capsule length, primary branches per plant, number of capsules on the main stem per plant, and total capsules per plant were among the features with high heritability and genetic advancement.

Sree *et al.* (2025) studied 44 genotypes of sesame and found that there were notable genotypic variations across the genotypes, according to analysis of variance. High GCV and PCV were observed for seed yield per plant, harvest index and number of capsules per plant. High heritability coupled with high genetic advance as percent of mean was observed for number of primary branches, seed yield per plant, number of capsules per plant, harvest index and height to first capsule.

12.3 Correlation coefficient

The relationship among important traits plays a crucial role in identifying desirable plant types from genetically diverse populations for effective breeding programmes. Improvement in yield is often more efficiently achieved through selection based on yield-contributing characters rather than direct selection for yield alone. In this context, Fryxell (1956) demonstrated that selection based on component traits was 250% more effective compared to selection based solely on yield. However, the association between characters may vary depending on the environmental conditions, the genetic material under study or both. Therefore, it is important to estimate the correlation among traits at both phenotypic and genotypic levels.

Sasipriya *et al.* (2022) evaluated fifty-one sesame genotypes and found that, at the genotypic and phenotypic correlation levels, seed yield per plant was positively correlated with the number of capsules per plant, 1000 seed weight, number of branches per plant, and number of seeds per capsule.

Durge *et al.* (2022) studied fifty-five sesame genotypes and observed revealed the number of capsules per plant had a significant positive association with seed yield, but the number of days to maturity had a strong negative correlation.

Kumar *et al.* (2022) evaluated 33 genotypes of sesame showed a strong and positive correlation with seed yield with respect to of the number of productive branches, the number of capsules per plant, the number of seeds per capsule, and the number of days to maturity.

Kumari and Shah (2023) conducted their experiment on thirty-six diverse genotypes of sesame and found a positive and significant correlation between seed yield per plant and plant height, internodal length, number of capsules per plant, number of branches per plant, stover production per plant, and harvest index.

Madhu *et al.* (2023) conduced their study on 106 genotypes of sesame and found a positive correlation between seed yield per plant and the number of capsules per plant (0.806) and 1000-seed weight (0.657).

Aye *et al.* (2024) studied 54 genotypes of sesame and reported that seed yield per plant was strongly associated with the number of primary branches, capsules per plant, and seeds per capsule.

Lakho *et al.* (2025) evaluated seven different sesame genotypes and revealed that oil content, days to initial flowering, plant height, and number of branches per plant both had a significant and positive correlation coefficient with seed produced.

Masoudi *et al.* (2025) conducted a experiment on total of 36 sesame genotypes and showed that the height of the first pod from the plant crown, seed weight of a capsule, biological yield, number of seeds in a capsule and plant height have the highest correlation coefficients with seed yield.

Sree *et al.* (2025) used 44 genotypes of Sesame used in the experiment, and it was shown that the number of capsules per plant, harvest index, oil content, and number of primary branches were all positively correlated with seed yield per plant.

12.4 Phenotypic stability analysis

The performance of genotypes within varied environments is often analysed in terms of stability. Adaptability is the ability of genotypes to remain consistently performing and to produce a relatively limited range of phenotypes in changing environmental conditions. The major objective of quantitative genetics is to measure the level of genetic variance, a level that can be used to predict the response to selection in breeding programmes. But the Genotype x Environment interaction can substantially affect the accuracy of variance estimates these interactions contribute to the random errors and can cause an overestimation of genetic variance. Consequently, missing differences between the expected and the actual response to selection can occur when the predictions are made using biased estimates of the genetic variance (Carvalho et al., 2016).

Genotypic performance varies markedly with fluctuations in environmental conditions. The effect of environment on phenotypic expression is evaluated by testing breeding materials across diverse environments and observing the resulting variations. Genotype × Environment interaction is a crucial factor in plant breeding programmes, and the ability of a genotype to exhibit stable

productivity over a wide range of environments is considered an important criterion for its release as a variety or hybrid.

According to Sprague (1966), G × E interaction is a measure of instability. Stability of any genotype means it will perform uniform under different environments. Environment fluctuations can be resisted by "well buffered" capacity of genotypes which shows stability in performance (Allard and Bradshaw, 1964 and Allard and Hansche, 1964). There is inverse relation between stability and genotype × environment interactions. The work done by various researchers has been reviewed under this section.

Kindeya *et al*. (2020) evaluated a total of seventeen white seeded sesame genotypes across six locations and found that there was significant variance in the mean oil yield amongst genotypes, ranging from 193.6 kg/ha for G8 to 409.4 kg/ha for G1. This variance among genotypes suggests that selection should be based on the mean oil yield performances of the genotypes to their individual conditions. The oil yield of genotypes varied to different environments.

Movahedi *et al.* (2020) studied a total of fifteen different sesame genotypes in 4 locations and observed that G4 > G6 > G1 > G2 were the stable genotypes with greater overall endurance. Jirouf 13 (G4), Darab 14 (G8), Safi Abad 1 (G9), Ahwaz Local Cultivar (G10), and Isfahan Local Cultivar (G13) were superior genotypes for seed yield and GEI impact based on the AMMI Stability Value (ASV) and Genotype Selection Index (GSI) and can be suggested for further research.

Azon *et al*. (2023) evaluated Eight environments and nineteen sesame accessions Two mega-environments for thousand seed weight and three mega-environments for days to 50% flowering and seed yield were displayed in the GGE biplot. In regard to seed yield, the most productive accessions in the first mega-environment were G11 and G13; in the second mega-environment, it was G10; and in the third mega-environment, it was G3 and G8. G10, G5, and G12 were found by AMMI and GGE investigations to be stable accessions with high seed yields in various settings. Based on their representativeness and discriminating power, GGE biplot showed that E1 and E2 were the best choices for multi-location trials.

Louise et al. (2025) sown twenty-two sesame accessions across three locations for two years and revealed that accession A15 stood out for its stability and good performance in all environments, making it the best performer.

12.5 Genetic diversity and molecular diversity

Assessment of genetic diversity is imperative in plant breeding to develop new cultivars or hybrids and also in the modification of the existing varieties to suit changing consumer preference. Molecular markers have an important potential of measuring genetic diversity by identifying polymorphisms, and they are extensively applied in various genomic studies for crop enhancement.

Genomic research has been highly reliant on molecular marker technologies. In the last three decades, there have been tremendous advancements in plant breeding, biochemistry and molecular biology with the emergence of marker systems. Molecular variation between and within the loci within a genome is high, in the form of nucleotide polymorphism. This variation depends on the species under investigation and significant variations can be found among the genes within the same genome (Nadeem *et al*.,2018).

Several polymerase chain reaction (PCR)-based marker systems such as RAPD, AFLP, RFLP and more advanced systems such as Simple Sequence Repeats (SSRs) and Single Nucleotide Polymorphisms (SNPs) have been successfully used to fingerprint sesame germplasm as well as to study genetic diversity.

Tesfaye *et al.* (2022) evaluated a total of 300 genotypes. Two high-throughput diversity array technology markers were used to genotype the panel. 5065 silicoDArT and 5821 SNP markers were aligned with the reference sesame genome out of the 6115 silicoDArT and 6474 SNP markers that were revealed. After filtering it using an allele frequency for every SNP site, 2997 high-quality SNPs remained for further research. Every genotype utilized in this investigation came from eight different geographic origins. The panel's average diversity was 0.14. Asia (0.17) was more diverse than Africa (0.14) at the continent level, but Africa collections (0.21) without Ethiopian collection were more diverse when geographical origin was taken into consideration. North Africa collections (0.23) were more diverse than others when Africa was further diversed. The genetic distance among the populations were ranged from 0.015 to 0.394.

Wang *et al.* (2023) evaluated 183 sesame accessions, including 101 Chinese cultivars, 62 landraces, and 20 exotic accessions, were analyzed using 25 pairs of simple sequence repeat (SSR) primers and 56 biological characteristics. There were 166 SSR polymorphic bands in all, with an average of 6.64 bands per marker, according to the analysis. Shannon's information index values showed a modest degree of genetic variety, ranging from 0.2732 to 0.6497. The range of the polymorphic information index was 0.0859 to 0.6357.

Seay *et al.* (2024) evaluated 24,735 high-quality Single-Nucleotide Polymorphism (SNP) markers were found throughout the 13 chromosomes after 501 accessions were examined. The average Polymorphism Information Content (PIC) value was 0.267, and the marker density was 1900 SNP per chromosome. According to Analysis of Molecular Variance (AMOVA), subpopulations contributed to 29.5% of the population's variation, whereas accessions within the subpopulations contributed 57.5%.

Maurya *et al.* (2025) performed the utilizing seven polymorphic SSR markers chosen from an initial screening consisting of 43 SSR markers, molecular diversity study utilizing SSR markers on a set of 2,496 sesame germplasms yielded a total of 140 alleles. Since the crop is self-pollinated (up to 35% outcrossing has been recorded, categorized as often cross-pollinated), the observed heterozygosity was lower than the expected heterozygosity. The population structure analysis divided the 2496 accessions into three main clusters or populations, but the molecular diversity analysis divided them into six clusters.

Parakhia *et al.* (2025) used Sequence-Related Amplified Polymorphism (SRAP) markers were used to examine genetic diversity among a group of thirty sesame accessions that represented various geographic contexts. A large number of alleles (1031) with 100% polymorphism were produced by combining 109 primers. The overall means for the SRAP Primer Index (SPI) and Polymorphic Information Content (PIC) were 8.09 and 0.83, respectively. With an average similarity score of 0.40 and genetic similarity values based on Jaccard coefficients ranging from 0.009 to 0.781, the examined accessions showed both a broad genetic basis and a large genetic distance.

12.6 Genome wide association studies

Association mapping studies in plants lead to identification of the genetic basis of variation caused by morphological, developmental and physiological change and it also provides a way to bring the researchers together for assembling of core collections and to develop genetic platforms for genotyping, phenotyping, analysis and interpretation (Sukumaran and Yu, 2014).

Zhou *et al.* (2022) grown a total of Three distinct settings were used to cultivate 400 sesame accessions. 43 important loci for Fatty Acid (FA) and Oil Content (OC) were found when the phenotypic data was linked to the recently published SNP data from whole-genome resequencing. 515 Differentially Expressed Genes (DEGs) were found across three stages of seed development using a comparative transcriptomics study of high-OC and low-OC materials. Twenty potential genes were found by combining the genome-wide association study (GWAS) and DEGs analysis; SiTPS1 (trehalose-6-phosphate synthase 1) has emerged as a crucial regulatory gene of FAs and TAGs metabolism in sesame. In transgenic Arabidopsis, overexpression of SiTPS1 affected FA composition and markedly raised OC.

Elsafy *et al.* (2025) used an Augmented Block Design to seed 200 genetically varied genotypes in two different habitats (Abu-Naama and Matuq). To analyze the genetic basis of the oleic acid, linoleic acid, and oil content, they used three Genome-Wide Association Study (GWAS) models: Multiple Locus Mixed Model [MLMM], Bayesian Information and Linkage-disequilibrium Iteratively Nested Keyway [BLINK], and fixed and random model Circulating Probability Unification [Farm CPU]. Because these qualities are quantitative, significant single nucleotide polymorphism (SNP) markers accounted for 3%–23% of the phenotypic variance across environments. Interestingly, all three models shared four SNPs (Chr1_1693157, Chr3_23284702, Chr5_17024932, and Chr9_1711873), indicating consistent and strong relationships between oleic acid and oil content. Four notable sequences were found to be associated with these loci by candidate gene analysis: a transcription repressor OFP8 (Sesamum alatum), an HVA22-like protein, a 3-oxoacyl-[acyl-carrier-protein] synthase 3 A, and a putative phospholipid diacylglycerol acyltransferase 2 in (S. indicum). These sequences may be important for oil biosynthesis and accumulation. Linoleic acid has also been

found to contain environment-specific loci, especially on chromosomes 6, 9, and 13.

Kefale *et al.* (2025) three conditions were used to grow 401 sesame accessions (2018WH, 2018LQ, and 2022WH). There were considerable differences in the oil and protein content of the sesame population. The oil content was between 41.68% and 60.15%, and the protein level was between 15.06% and 26.45%. Additionally, there was a correlation between seed color and oil and protein content, with the white seeds having a greater oil content and the black seeds having a higher protein level. 632 and 269 QTLs were identified as significant genetic areas for protein and oil content, respectively, according to GWAS data. We found 10 and 22 stable QTLs for protein and oil content, respectively, out of these important QTLs. Within 32 stable quantitative trait loci (QTLs), 17 potential genes associated with protein and oil content were found. It's interesting to note that the gene sequences of SINPZ1300586 and SINPZ1300694 contained two variation sites related to protein content, SNP13:10093594 and InDel13:10935497. The genes SINPZ0102106, SINPZ0401222, SINPZ0801731, and SINPZ1100015 are associated with four SNPs for oil content: SNP1:22608987, SNP4:13355820, SNP8:21686488, and SNP11:142842.

Gebeyehu and Ortiz (2026) identified 36 significant relationships, including novel loci on chromosomes 12 and 13 not reported in Asian-focused research, were found by using GWAS on 200 Ethiopian accessions, represented by 3683 SNPs. Key hormonal and transcriptional mechanisms were implicated by candidate genes assigned to these loci: transcription factors (WRKY23, DOF3.1, and SBP-like) modulate flavonoid pathways controlling seed coat pigmentation, while brassinosteroid biosynthesis (CYP90B1) and ethylene signaling (AP2/ERF) likely regulate plant architecture. Two separate groups were identified by population structure analyses (K = 2), and linkage disequilibrium (LD) declined fast (~190 kb), enabling fine mapping.

Gelashe *et al.* (2026) DArTSeq-based SNP markers were used to evaluate population structure and genome-wide genetic diversity in 188 sesame accessions from six Ethiopian Agricultural Research Centers. Methods: Out of the initial sample of 12,302 SNPs, 5163 high-quality markers were kept after quality filtering. Because sesame is primarily self-pollinating, the mean anticipated heterozygosity

(He = 0.201) was higher than the observed heterozygosity (Ho = 0.193). The SNPs were distributed unevenly among 16 linkage groups, with a transition/transversion ratio of 1.17:1. An obvious hierarchical population structure with discrete clusters and variable admixture was shown using STRUCTURE, PCA, DAPC, and neighbor-joining cluster analysis. While Werer (WARC) and Gambella (GaARC) were significant diversity repositories with substantial heterozygosity and gene diversity, accessions from Assosa (AARC) and Bako (BARC) were genetically homogeneous.

Materials and methods

The experimental material will be comprised 150 sesame genotypes collected from ARS, Amreli of which 100 genotypes will be selected for further study. All genotypes will be evaluated during two seasons and at two locations i.e., *Kharif* 2026 and Summer 2027 at Junagadh and Amreli.

12.1	**Year and Season of experiment**	:	A) Screening: *Kharif 2026* B) Evaluation: Summer 2026,2027 *Kharif* 2026,2027
12.2	**Total number of environments**	:	Four (4)
12.3	**Screening season**	:	Summer 2026
12.4	**Evaluation location**	:	a) Sagdividi Farm, Department of Seed Science and Technology JAU, Junagadh b) Agriculture Research Station, Amreli
12.5	**Experimental Design**	:	Alpha Lattice Design
12.6	**No. of Replications**	:	Two (2)
12.7	**Spacing**	:	30 cm × 10 cm in 60 cm × 10 cm in
12.8	**Treatment Details**	:	100 genotypes out of 150 genotypes selected for further study

12.7 List of Genotypes

No.	Genotype	No.	Genotype	No.	Genotype	No.	Genotype	No.	Genotype
1	Nana Bhumodaru-5	**16**	NIC-12336	**31**	IC-17326	**46**	Pipariyu-4	**61**	IC-204854
2	Hathigudh 1-2	**17**	Junagadh collection-1	**32**	IC-204495	**47**	Vijapadi-13	**62**	Kalyanpur-1
3	Hathigudh 1-1	**18**	NIC-12509	**33**	IC-204500	**48**	IC-23274	**63**	IC-26304
4	Ingoralu-5	**19**	NIC-12345	**34**	KMR-77	**49**	Nana gokharvala-3	**64**	Gavadka-1
5	Lalavadur-6	**20**	IC-43063	**35**	IC-9987	**50**	Ziru-1	**65**	Kundia-6
6	Bhingral-5	**21**	NIC-8486	**36**	IC-19274	**51**	Nana Bhamodara-7	**66**	IC-19248
7	Motaliliya-2	**22**	IC-20528	**37**	IC-204653	**52**	IC-14082	**67**	IC-42952
8	TNAU-12	**23**	IC-199433	**38**	IC-204496	**53**	Pipariyu-2	**68**	Gavadka-5
9	Hathigudh-1-3	**24**	NIC-8526	**39**	IC-132186	**54**	TC-359	**69**	IC-12483
10	Chavand-1	**25**	KMR-69	**40**	KMR-102	**55**	Sel. 91-1	**70**	RT-125
11	Nana Bhamodara-6	**26**	NIC-8476	**41**	KMR-92	**56**	Kalyanpur-3	**71**	OMT-32
12	Songadh	**27**	NIC-9858	**42**	IC-12335	**57**	IC-43116	**72**	Borda-1
13	Nand Bhamodara-1	**28**	IC-127278	**43**	IC-20526	**58**	DC-67-34	**73**	Gavadka-11
14	Khadkala-8	**29**	IC-204681	**44**	DS-67-74	**59**	Zira-3	**74**	Borda-2
15	NIC-13598	**30**	IC-12389	**45**	IC-199435	**60**	JLT-35	**75**	IC-23309

No.	Genotype	No.	Genotype	No.	Genotype	No.	Genotype	No.	Genotype
76	IC-43036	91	EC-346896	106	DTDS-25-3	121	DS-25-28	136	TC-150
77	Pipariya-1	92	RMT-711	107	RMT-686	122	TPTS-80	137	SS-62
78	Amreli-sel-91-3	93	JCS-3755	108	VS-20-008	123	TPTS-64	138	SPS-13
79	IC-54035	94	JCS-3888	109	IC-205729	124	MT-6725	139	DC-28
80	AST-9	95	TPTS-71	110	TKG-23-14	125	Kalyanpur-8	140	IS-209
81	X-62-10	96	DSTS-25-25	111	RMT-695	126	SPS-4	141	HT-15
82	Saladi-2	97	RMT-675	112	RMT-631	127	DC-26	142	DC-29-5
83	IC-124761	98	PCU-24-21	113	TKG-23-03	128	SI-795	143	Tape-13
84	Kalyanpur-4	99	RMT-586	114	TPTS-59	129	Ansodar-2	144	IS-222
85	Kundia-5	100	RMT-661	115	IC-204067	130	Gundran	145	ES-72
86	Nunu Bhamodara-4	101	TPTS-06	116	TPTS-01	131	JT-1	146	DC-29
87	IC-23207	102	PCU-24-6	117	RMT-708	132	DPI-144	147	ES-22
88	Khijadiya-1	103	TPTS-46	118	VS-21-078	133	NU-34-1	148	DC-76
89	DC-27	104	RMT-677	119	IC-205547	134	G.Til-10	149	DC-19-43
90	Nana Gokharvala-1	105	RMT-660	120	RMT-705	135	SPS-34	150	DC-11

12.11 Observations to be recorded

Observations will be recorded on five randomly selected competitive plants of each entry in each replication for various characters. The days to 50 per cent flowering and days to maturity will be recorded on plot basis while rest of the observations will be recorded from five randomly selected competitive plants of each genotype from each replication. The details of the procedure to be followed for recording data for various characters are described below.

12.11.1 Days to 50 % flowering

The days to 50% flowering will be recorded on a plot basis as the number of days taken from sowing to the stage when 50% of plants in the plot have at least one open flower.

12.11.2 Days to maturity

Number of days taken from sowing to 80% maturity. The total number of days taken from sowing to complete maturity was recorded as days to maturity."

12.11.3 Plant height

Height of the five randomly selected plants in each experimental unit was measured in centimetres from bottom to the apical tip of the plant at the time of harvesting and mean plant height for each genotype in individual replication was computed.

12.11.4 Number of branches per plant

The observation was recorded by counting the total number of branches presented on main stem of five randomly selected plants of each experimental unit of a replication at the time of harvesting.

12.11.5 Number of capsules per plant

Total capsules borne by each randomly selected plants of an experimental unit of a replication were counted and recorded accordingly, mean was worked out for each experimental unit.

12.11.6 Capsule length (Cm)

The length of five matured non-shattered capsules selected at random from each plant was recorded and the mean was expressed in centimeters.

12.11.7 Number of seeds per capsule

Seeds of five capsules at various heights were harvested when seeds were intact from each sample and the mean number of seeds per capsule was recorded by

counting all the seeds to number of capsules.

12.11.8 Test weight (g)

Weight of 1000 fully mature dry seeds will be measured in grams on an electronic balance up to the two decimals.

12.11.9 Seed yield per plant(g)

The seed produced from each of the randomly selected plant of an experimental unit was bulked and weighted in gram. An average was worked out as seed yield per plant.

12.11.10 Disease scoring assessment and classification

a) **Screening**: Disease scoring will be undertaken for *Macrophomina* root rot resistance were scored under sick plot condition in screening stage by using 0-9 scale by Mayee and Datar, 1986.

b) **Evaluation:** the observations again in the evaluation phase will be taken under natural condition by using by using 0-9 scale by Mayee and Datar, 1986.

The severity of root rot caused by *Macrophomina phaseolina* will be assessed using a standard disease rating scale. Percent disease incidence (PDI) will be calculated and genotypes will be categorized into resistant, moderately resistant, susceptible and highly susceptible groups based on disease reaction (Mayee and Datar, 1986).

Score	Disease Severity (%)	Reaction Category	Description
0	0	Immune (I)	No visible symptoms
1	1–10	Resistant (R)	Very slight infection
3	11–25	Moderately Resistant (MR)	Small lesions, limited spread
5	26–50	Moderately Susceptible (MS)	Noticeable infection, partial damage
7	51–75	Susceptible (S)	Severe infection, significant plant damage
9	76–100	Highly Susceptible (HS)	Very severe infection, plant death or near death

Per cent Disease Index (PDI) =

$$\frac{\text{Sum of all disease ratings}}{\text{Total number of observations} \times \text{Maximum disease grade}} \times 100$$

13. Statistical analysis

The mean values of all the genotypes for all the characters will be subjected to statistical analysis in the following aspects:

13.1 Analysis of variance for experimental design

The analysis of variance for the experimental design will be carried out in Alpha Lattice Design for all the characters as per Patterson and Williams (1976).

13.2 Variability parameters

The variability parameters *viz*., genotypic coefficient of variation and phenotypic coefficient of variation will be estimated as per the procedure suggested by Burton (1952). The heritability and genetic advance will be calculated as per procedure suggested by Allard (1960).

13.3 Correlation coefficients

The genotypic and phenotypic correlations will be worked out as per procedure suggested by Al-Jibouri *et al*. (1958).

13.4 Phenotypic stability analysis

G × E interaction and stability analysis will be carried out as AMMI model and GGE biplot.

13.5 Genetic diversity and molecular diversity

Cluster analysis using molecular markers data will generate tree through suitable method.

13.6 Genome wide association studies

Association between the marker and the trait was analyzed using suitable version of TASSEL software.

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Signature of Student	Signature of Major Guide
(Sanapala. Sai Harshavardhan)	(Lata J. Raval)